SEQUENCE LISTING

<110> REFF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO

<120> GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS

<130> 23522.0699

<140> 09/292,053
<141> 1999-04-14

<150> 08/803,085
<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
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<221> mat_peptide
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<220>
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<222> (1)..(390)

<400> 1

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atg gcc tgg act ctg ctc ctc gtc acc ctc ctc act cag ggc aca gga   48
Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly
                -15                 -10                 -5

tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct   96
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser
        -1   1               5                  10

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt   144
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
    15                  20                  25

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc   192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
 30                  35                  40                  45

ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct   240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
                50                  55                  60
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gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc   288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
            65                  70                  75

tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat   336
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
        80                  85                  90

aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc   384
Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
    95                  100                 105

cta ggt
Leu Gly                                                          390
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<210> 2
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<213> Homo sapiens

<400> 2

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Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly
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Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser
        -1   1                   5                  10

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
    15                  20                  25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
30                  35                  40                  45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
                50                  55                  60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
            65                  70                  75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
        80                  85                  90

Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
    95                  100                 105

Leu Gly
110
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<210> 3
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<212> DNA
<213> Homo sapiens

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<222> (1)..(58)

<220>
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<222> (58)..(423)

<220>
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<222> (1)..(423)

<400> 3

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atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg   48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
               -15                 -10                 -5

gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga gtg gtg aag   96
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
        -1   1               5                  10

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc   144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
     15                  20                  25

agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga   192
Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
 30                  35                  40                  45

ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac   240
Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
                50                  55                  60

aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag   288
Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
            65                  70                  75

aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc   336
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
        80                  85                  90

gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta   384
Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
     95                  100                 105

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca               423
Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
110                 115                 120
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<210> 4
<211> 141
<212> PRT
<213> Homo sapiens

<400> 4

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
               -15                 -10                 -5
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```
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
         -1   1                5                  10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
     15                  20                  25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
 30                  35                  40                  45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
                 50                  55                  60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
             65                  70                  75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
         80                  85                  90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
     95                  100                 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
110                 115                 120
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<210> 5
<211> 387
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<213> Homo sapiens

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<222> (1)..(387)

<400> 5

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atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg   48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
        -20                 -15                 -10

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc   96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
     -5              -1   1                5                  10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt   144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
                15                  20                  25
```

```
cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa   192
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
            30                  35                  40

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc   240
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
        45                  50                  55

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc   288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
    60                  65                  70

gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag   336
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
75                  80                  85                  90

gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc   384
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
                95                  100                 105

aaa                                                               387
Lys
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<210> 6
<211> 129
<212> PRT
<213> Homo sapiens

<400> 6

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
       -20                 -15                 -10

Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    -5              -1   1                   5                  10

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
                15                  20                  25

Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
            30                  35                  40

Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
        45                  50                  55

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
    60                  65                  70

Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
75                  80                  85                  90

Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
                95                  100                 105

Lys
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<210> 7

<211> 411
<212> DNA
<213> Homo sapiens

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<222> (1)..(411)

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atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt cct ctt ttg aaa ggt   48
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
                -15                 -10                 -5

gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag   96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
         -1   1               5                  10

cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc   144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
     15                  20                  25

acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag   192
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30                  35                  40                  45

ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg   240
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
                50                  55                  60

tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc   288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
            65                  70                  75

aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg   336
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
        80                  85                  90

gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc   384
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
    95                  100                 105

cag gga gtc ctg gtc acc gtc tcc tca                              411
Gln Gly Val Leu Val Thr Val Ser Ser
110                 115
```

<210> 8
<211> 137
<212> PRT
<213> Homo sapiens

<400> 8
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
-15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
-1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
65 70 75

Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
80 85 90

Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
95 100 105

Gln Gly Val Leu Val Thr Val Ser Ser
110 115

<210> 9
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
atcacagatc tctcaccatg gacatgaggg tccccgctca g 41

<210> 10
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
atcacagatc tctcaccatg aggctccctg ctcag 35

<210> 11
<211> 35
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
atcacagatc tctcaccatg gaarccccag ckcag 35

<210> 12
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
atcacagatc tctcaccatg gtgttgcaga cccaggtc 38

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
ggtgcagcca ccgtagcttt gatytccasc tt 32

<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
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<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
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<210> 16

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
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<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
cttgggctga cctaggacgg t 21

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
gcgactaagt cgaccatgga ctggacctgg 30

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
gcgactaagt cgaccatgaa acacctgtgg 30

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gcgactaagt cgaccatgga gtttgggctg agc 33

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gcgactaagt cgaccatggg gtcaaccgcc atc 33

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
gcgactaagt cgaccatgtc tgtctccttc ctc 33

<210> 23
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
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<210> 24
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<212> DNA
<213> Artificial Sequence

<220>
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gatgggccct tggtgctagc tgaggagacg g 31

<210> 25
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
atttaggtga cactata 17

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gttttcccag tcacga 16

<210> 28
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 28
atatacgact cactataggg 20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
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<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<210> 31
<211> 21
<212> DNA
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<220>
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ccaggccact gtcacggctt c 21

<210> 32
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 32
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<210> 33
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
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<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
acacagaccc gtcgacatgg 20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
gctctcggag gtgctcctgg 20

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
acagacccgt cgaccatgga gtttgggctg 30

<210> 37
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 37
ccccttggtg ctagctgagg agacggt 27

<210> 38
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
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<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
aaacagtgtg ttcttggcgt tctctct 27